

عنوان مقاله:

Genetic markers and smoking status

محل انتشار:

سومین کنگره ملی دخانیات و سلامت (سال: 1397)

تعداد صفحات اصل مقاله: 2

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خلاصه مقاله:

Smoking is one of the most harmful behaviors linked with harmful health conditions in smokers and passive smokers. Smoking has ۳ stages: initiating, current smoking and smoking cessation. This behavior is a multistep process with genetic influences. Current review focuses on loci associated with smoking behavior and predictive epigenetic biomarkers for smoking status. NTRK γ is associated with smoking initiation and dependence. BDNF binds with NTRK and reinforces nicotine dependence and smoking behavior. The tobacco and genetics (TAG) consortium reports variants at the BDNF locus influence smoking initiation. A region on chromosome ۱۵ (۱۵q۲۵) including the nicotinic receptor subunit genes CHRNA۵, CHRNA۳ and CHRNBF (encoding NAChr receptors) was associated with cigarettes consumed per day (CPD), a measure of smoking dependence. The TAG and european network for genetic and genomic epidemiology (ENGAGE) consortia also identified the CHRNA۶-CHRNBF cluster on chromosome ۸p۱۱, as well as loci found near CYP2A۶ on ۱۹q۱۳ and in a region containing noncoding RNAs on chromosome ۱۰q۲۳ and ۱۰q۲۵, as associated with CPD with unknown function. Association of CHRNA۶ with smoking behavior was reported previously in a candidate gene study and is consistent with the gene's high expression in dopamine-releasing neurons (which have a key role in smoking). For smoking cessation, the TAG consortium identified a region on chromosome ۹ near the gene encoding dopamine β -hydroxylase (DBH) which catalyzes the conversion of dopamine to norepinephrine. Polymorphisms of cytochrome p۴۵۰۲A۶ (encoded by CYP2A۶) strongly influence the catabolism of nicotine into inactive metabolites, and individuals with rapid metabolism require higher levels of smoking to maintain the same nicotine level than do individuals whose genotypes confer slower metabolism. Epigenome-wide association studies (EpWAS) in Europe revealed that LRRN۳ (among CpG sites) had increased expression and methylation and could be a biomarker for smoking status. EpWAS results in comparing nonsmokers and smokers show ۳ different loci on the AHRR gene (chromosome ۵) (P-values from ۱۰-۱۰۶ to ۱۰-۱۴), ۴ CpG sites in a non-annotated region on chromosome ۲ (۲q۳۷.۱), ۵ sites on chromosome ۱ (including ۴ sites on GFI۱ and ۱ on GNG۱۲), ۱ CpG site on chromosome ۱۹ (F۲RL۳), ۱ CpG site in a non-annotated region on chromosome ۶ (۶p۲۱.۳۳) and ۳ CpG sites on

chromosome ۱۱ (KCNQ1OT1), ۱۲ (RARG) and ۱۶ (ADCY9), respectively. Hypomethylation at CpG sites on AHRR and ... GFI1 in new-born cord blood related is related to maternal smoking. Several hyper

کلمات کلیدی:

Smoking, Gene, Expression, Biomarker, Epigenetics

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